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Morphological Characterization of Bullock's Heart (*Annona Reticulata* L.) Germplasm in Konkan Region of Maharashtra State (India)

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Abstract: *Annona reticulata L. is an underutilized fruit tree species in Maharashtra (India), which is mostly confined to homegardens. Despite the importance of A. reticulata, collection, characterization and improvement of its germplasm is limited in Maharashtra (India), hence hindered its effective conservation and utilization. Therefore, the objective of this research was to identify morphological variation of A. reticulata populations in Maharashtra (India). Multistage Sampling Survey was conducted in homegardens of Ratnagiri and Sindhudurg districts of Maharashtra (India) during the year 2012 and 2013. Morphological variation of A. reticulata were observed on total of 100 samples collected from eleven tahsils of two districts. A total of eighty three both morphological and bio-chemical characteristics were measured and used to analyze in this study. Among this, five morphological characters did not show any variance in 100 genotypes and accordingly removed from the analysis. Finally leaving 78 characters to be subjected to Principal Component Analysis (PCA) and Factor Analysis (FA), followed by Cluster Analysis. A dendrogram of evaluated characters showed eleven distinguished clusters. Implications of findings are discussed in relation to utilization and conservation.*

Keywords: *Annona reticulata, cluster analysis, factor analysis, homegardens, morphological variations*

INTRODUCTION

Annona reticulata L. of the family Annonaceae (commonly known as *Bullock's heart* or *Ramphal*) is one of the world's most exquisite, but less studied fruit species in Maharashtra (India). The fruits are consumed widely as fresh form and the other plant parts are also a source of medicinal and other industrial products such as beverages, wine, jellies, jam and fruit-butter preserves and pure (Gleye *et al.*, 1997 [3]; Pinto *et al.*, 2005 [10]; Heenkenda *et al.*, 2011) [5]. The fruits contain vitamins, minerals, bio-active chemical substances. The other plant parts also contain numerous amounts bio-active chemical substances such as acetogenins, alkaloids, terpens, flavonoids, cyclopeptide annomuricatin and oils (Roblot *et al.*, 1993 [13]; Gleye *et al.*, 1999 [4]; Pinto *et al.*, 2005) [10]. These compounds are very useful medicines because some acetogenins have antitumoral, insecticidal, antibacterial, immuno-suppressant, pesticidal or antihelminthic properties (Kim *et al.*, 1998 [8]; Yu *et al.*, 1998) [18].

However, in India *A. reticulata* is categorized as an underutilized fruit tree species (Heenkenda *et al.*, 2011) [5]. Only a limited amount of researches has been conducted on *Annona* species in India, though this species in general has high potential to diversify the farming system (Bowe and Haq, 2010) [2].

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Morphological characterization of a species is very useful in the separation of populations into different morphotypes and proper utilization of genetic resources in plant breeding programmes (Piyasundara *et al*., 2009) [12]. Better understanding of genetic diversity present and its distribution is essential for rational utilization of germplasm in crop improvement (Piyasundara *et al*., 2009) [12]. Study of plant genetic resources are also important to identify agro-biodiversity and this include primitive forms of cultivated plants, modern cultivars, *ex-situ* collections and related wild species. Genetic diversity created in farmers' fields, homegardens over millennia (Upadhyaya *et al*., 2008) [17]. The objectives of the present research were identification of morphological variation of *A. reticulata* population in homegardens in south Konkan region of Maharashtra state (India).

MATERIAL AND METHODS

Data Collection for *A. Reticulata* Trees

Tree of *A. reticulata* is found mainly in homegardens of many parts of India except in the higher elevations (Pinto e*t al.*, 2005) [10] and eleven *ex situ A. reticulata* gemplasm collections are located in two district of South Konkan region of Maharashtra state. Sampling of homegardens was done using the multistage sampling method to conduct the survey in large geographical area in the South Konkan region. In order to increase the precision of sampling a large number of clusters were used as Thattil (1999) [15] and Thattil and Samita, (2007) [16] suggested. Since a descriptor list for *A. reticulata* is not available, the descriptor list of *A. cherimola* Mill. (Cherimoya) compiled by the International Plant Genetic Resources Institute (IPGRI, 2008) [7] was used in this study. A total of eighty three (83) both morphological and bio-chemical descriptors were measured and used to analyze in this study.

Among 83 characters, 5 morphological characters did not show any variance in 100 genotypes and accordingly removed from the analysis namely; suckering tendency, pubescence of upper surface, pubescence of lower surface, colour of young leaves and colour of stigma Accordingly, 78 morphological descriptors including thirty eight quantitative and twenty two qualitative descriptors and 18 bio-chemical descriptors were identified and assessed. From each tree ten fully expanded and healthy leaves, ten flowers and two well-developed fruits were randomly selected for measurements of characters.

Twenty two qualitative characters were categorized and measured (Table 2). Munsell Color System chart has been published by *Azalea Society of America* (Anon., 1999) [1] was used to identify parameter such as trunck colour, Colour of young branches, leaf colour, flower colour, exocarp color, pulp colour and seed colour.

Data Analysis (Multivariate/Biometrical Analysis)

The observations were taken on plant and plot basis as per descriptor's list of *A. cherimola* published by IPGRI, 2008 which included quantitative and visual characters both. Non-parametric data were converted to scales as proposed by IPGRI in descriptors for *A. cherimola* (IPGRI, 2008) [7]. A total of 100 samples were collected from eleven tahsils of two districts and analysed. The multivariate analysis, namely Principal Component Analysis (PCA), Factor analysis (FA) and Hierarchical cluster Analysis (HCA), as developed by Mahalanobis (1936), were performed using the mean data for each character and pooled value of bio-chemical characters following the widely used Windostat version 9.1 and JMP@10.0.2 statistical computer software packages program. In order to identify the extent of variability of the genotypes included in the study, the effect that the various analyzed traits have on the expressed variability and to classify the genotypes based on their variability, the above statistical analyses were performed.

For aforementioned multivariate (biometrical) analysis, total 65 characters were used out of 78 characters and remaining 13 characters including trunk colour, tree girth, colour of young branches, defoliation at end of the fructification phase, shape of leaf base, shape of leaf apex, leaf petiole length, colour of mature leaves, leaf margin, leaf blade venation, colour of the internal petal base, pulp colour and seed coat colour were also removed from the analysis due to low coefficient of variation (Table 1 and 2 show such variables using asteric*). Further more, among 65 characters, 11 morphological

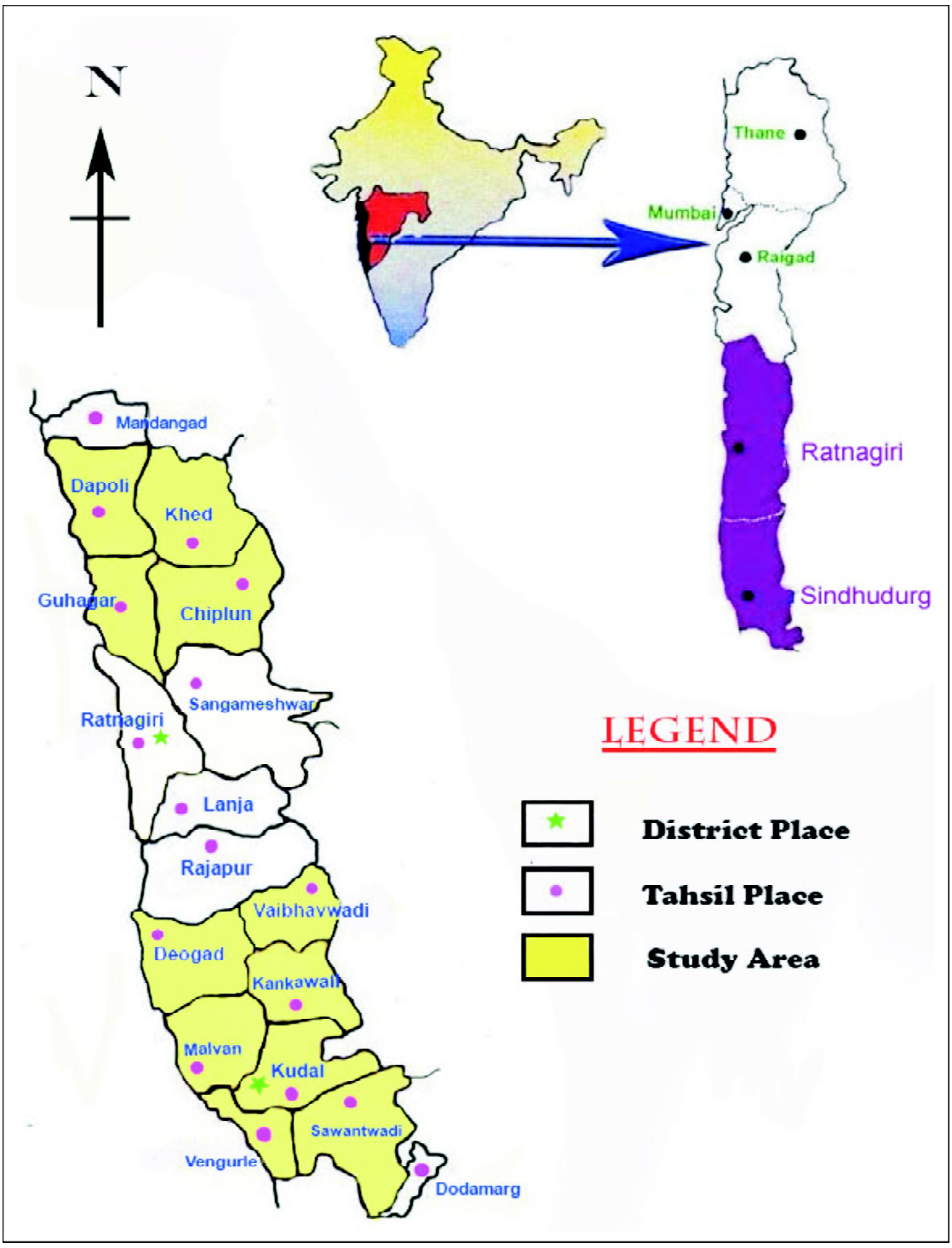

Figure 1: Distribution of sampling sites (selected districts) in Maharashtra

qualitative, 36 morphological quantitative and 18 bio-chemical parameters were analyzed separately. The collected data were summarized and subjected to diversity analysis.

Principal Component Analysis (PCA) and Factor Analysis (FA) were carried out using average values of descriptors. The results were used for cluster analysis. The analysis was conducted using Statistical Analysis System (SAS) for Windows Version 9.1 and JMP@10.0.2. The PCA and FA were used conducted for total data set. Eigen values greater than 1.00 and cumulative proportion of

Table 1
Variation of quantitative characters measured and used in the analysis

Quantitative characters	*Mean*	*SD*	*CV*	*S.E.±*	*Variance*
Canopy spread (m)	8.90	1.45	16.32	0.15	2.11
Tree height (m)	10.67	2.49	23.38	0.25	6.22
*Trunk girth (cm)	57.34	20.65	36.02	2.07	426.62
Trunk ramification	2.0	0.71	35.53	0.07	0.51
Leaf length (cm)	16.17	1.62	10.01	0.16	2.62
Leaf width (cm)	4.53	0.48	10.69	0.05	0.23
Leaf length: width ratio	3.60	0.43	12.02	0.04	0.19
*Petiole length (cm)	1.78	0.19	10.86	0.02	0.04
Leaf area (cm^2)	41.89	1.84	4.40	0.18	3.40
Flower length (cm)	2.36	0.18	7.79	0.02	0.03
Flower diameter (cm)	2.69	0.28	10.48	0.03	0.08
Peduncle length (cm)	3.20	0.45	14.00	0.04	0.20
Pedicel length (cm)	2.60	0.38	14.44	0.04	0.14
Petal length (cm)	2.49	0.13	5.22	0.01	0.02
Petal breadth (cm)	0.54	0.05	9.41	0.01	0.00
Fruit weight at harvest (g)	362.21	82.07	22.66	8.21	6735.77
Yield (fruits/tree)	41.37	11.80	28.53	1.18	139.29
Fruit length (cm)	8.63	1.48	17.10	0.15	2.18
Fruit diameter (cm)	8.80	1.30	14.78	0.13	1.69
Fruit girth (cm)	24.44	2.12	8.68	0.21	4.50
Days from harvest to ripening	5.37	1.06	19.74	0.11	1.12
Weight of ripe fruit (g)	347.58	82.29	23.68	8.23	6771.74
Fruit volume (ml)	314.84	81.86	26.00	8.19	6700.51
Fruit specific gravity	1.16	0.06	5.23	0.01	0.00
Fruit rind weight (g)	155.50	32.71	21.04	3.27	1069.9
Fruit rind percent (%)	45.58	7.11	15.59	0.71	50.52
Fruit rind thickness (mm)	2.90	0.46	15.98	0.05	0.21
Fruit receptacle length (cm)	4.45	0.67	15.05	0.07	0.45
Fruit receptacle weight (g)	4.85	0.60	12.38	0.06	0.36
Fruit receptacle percent (%)	1.47	0.38	25.59	0.04	0.14
Pulp weight (g)	165.37	62.55	37.82	6.26	3912.73
Pulp percent (%)	46.34	7.92	17.09	0.79	62.76
No. of seeds per fruit	71.46	15.90	22.25	1.59	252.88
Weight of seeds (g)	21.83	5.34	24.45	0.53	28.49
Seeds:Pulp	0.15	0.06	43.07	0.01	0.00
Seed percent (%)	6.61	2.23	33.75	0.22	4.97
Seed length (cm)	1.53	0.04	2.79	0.00	0.00
Seed width (mm)	7.57	0.75	9.86	0.07	0.56
PLW (%) (Harvest to ripening)	4.28	1.20	28.13	0.12	1.45
Moisture (%)	71.19	3.06	4.30	0.31	9.38
Total soluble solids (^{o} B)	28.73	1.73	6.03	0.17	3.00
Titratable acidity (%)	0.24	0.06	26.65	0.01	0.00
pH	4.26	0.43	10.01	0.04	0.18
TSS:TA	135.6	51.58	38.05	5.16	2660.9

Cont. table 1

Quantitative characters	*Mean*	*SD*	*CV*	*S.E.±*	*Variance*
Reducing sugars (%)	15.06	1.37	9.12	0.14	1.89
Non-reducing sugars (%)	4.24	0.64	15.10	0.06	0.41
Total sugars (%)	19.30	1.93	10.00	0.19	3.72
Ascorbic acid (mg $100g^{-1}$)	23.72	4.01	16.92	0.40	16.11
Carbohydrate (%)	26.74	1.25	4.66	0.12	1.56
Protein (%)	0.92	0.10	10.72	0.01	0.01
Crude fibre (%)	1.20	0.12	9.71	0.01	0.01
Fat (%)	0.57	0.12	21.53	0.01	0.01
Shelf life (days after ripening)	3.75	0.59	15.75	0.06	0.35
Organoleptic colour score	7.62	0.60	7.82	0.06	0.35
Organoleptic flavour score	7.42	0.53	7.11	0.05	0.28
Organoleptic texture score	6.41	0.49	7.58	0.05	0.24

(* indicated characters with no variation.) (*Pooled data*)

Table 2
Variation of qualitative descriptor's measured and used in the analysis

Qualitative parameters	*Observed Variation*
*Trunk colour	1. Light grey (43%), 2. Dark grey (40%) and 3. Pale grey (17%).
Tree crown shape	1. Ellipsoid (11%), 2. Spheroid (9%), 3. Oblong (42%) and 4. Irregular (38%).
Tree growth habit	1. Erect (64%), 2. Spreading (8%), 3. Semi-spreading (28%) and 4. Drooping (0%).
*Colour of young branches	1. Light green (37%), 2. Dark green (24%), 3. Moderate green (18%) and 4. Pale green (21%).
*Defoliation at the end of fructification phase	0. Absent (0%), 1. Partial (82%) or 3. Complete (18%).
Leaf blade shape	1. Ovate (15%), 2. Elliptic (19%), 3. Obovate (0%) and 4. Lanceolate (66%).
*Shape of leaf base	1. Acute (87%), 2. Rounded (13%), 3. Obtuse (0%) and 4. Cordate (0%).
*Shape of leaf apex	1. Acute (85%), 2. Rounded (0%) and 3. Acuminate (15%).
*Colour of mature leaves	1. Light green (23%), 2. Brilliant green/Green (23%), 3. Greyish green (0%) and 4. Dark green (54%).
*Leaf margin	1. Entire (100%) or 2. Undulated (0%).
*Leaf blade venation	3. Submerged (0%), 5. Intermediate (100%) or 7. Raised (0%).
Petal outer colour	1. Yellowish green (55.0%), 2. Light yellowish green (30.0%), 3. Deep yellowish green (15.0%) and 99. Other (0%).
*Colour of the internal petal base	1. Pink (63%), 2. Light reddish purple (11%), 3. Dark red (26%) and 4. Deep reddish purple (0%).
Location of fructification	1. Base of the crown (10%), 2. Middle of the crown (71%) and 3. Top of the crown (19%).

Cont. table 2

Qualitative parameters	*Observed Variation*
Fruit shape	1. Round (10%) 2. Oblate (6%) 3. Cordate/Heart (60%) 4. Broadly cordate (17%) 5. Oval (7%).
Fruit symmetry	0. Asymmetric (40%) or 1. Symmetric (60%).
Uniformity in fruit size	0. No (48%) or 1. Yes (52%).
Fruit exocarp type	1. *Laevis* (smooth) (65%), 2. *Impressa* (slight depressions) (33%), 3. *Umbonata* (small protrusions) (2%), 4. *Tuberculata* (medium protrusions) (0%) and 5. *Mamillata* (large protrusions) (0%).
Ripe fruit colour	1. Reddish yellow (32%), 2. Reddish brown (52%), 3. Reddish green (13%) and 4. Pink (3%).
*Pulp colour	1. White (0%) and 2. Creamy white (100%).
Pulp texture	1. Watery (46%), 2. Creamy (30%), 3. Granular (24%), 4. Hard (0%) and 5. Hard areas in the pulp (%).
*Seed coat colour	1. Grey (0%), 2. Brownish black/Dark brown (28%), 3. Black (72%) and 99. Other (0%).

(* indicated characters with no variation)

variation explained were used to identify number of principal components (Thattil and Samita, 2007) [16]. The magnitudes of the component coefficients in Eigen vectors were used to measure the importance of each character to the particular principal component. Cluster analysis is the partitioning of a set of objects into groups so that objects within a group are similar and objects in different groups are dissimilar. It is efficient in grouping objects with similar characters (Hodgkin *et al*., 1995) [6].

The analysis was performed using the cluster procedure (method = Ward's minimum distance method) and the dendrogram with the tree procedure of SAS. Previous studies have shown that the average linkage and Ward's minimum distance method was used by many researchers in cluster analysis studies (Piyasiri *et al*., 2001 [11]; Ruckshanthi *et al*., 2002 [14]; Piyasundara *et al*., 2009) [12]. Clusters were defined based on their unique characters. In order to identify the relationship of accessions, they were plotted using variables (*i.e.* PC 1 *vs.* PC 2) as shown in Figure 2 Correlations among characters were identified using two dimensional plotting of factors (Figure 3).

RESULTS AND DISCUSSION

The data shown in Table 3 with regards to factor analysis revealed that FA identified 5 factors retained by positive eigen value criterion, explained 150.85% of the total genotypes variation and FA performed most of the variability of the analyzed genotypes has been explained by first 3 factors. 1st two factors together explained 100.05% of the variance among the genotypes. First factor with eigen value of 1.10 accounted for 62.70% of the variation and is primarily related to uniformity in fruit size, fruit symmetry, tree growth habit and ripe fruit colour, while uniformity in fruit size, fruit symmetry, and ripe fruit colour showed highest positive correlation. The 2nd factor that accounted for 37.35% of the total variance and is mainly loaded by fruit exocarp type, fruit symmetry, leaf blade shape and petal outer colour, while fruit symmetry and leaf blade shape revealed highest positive correlation. The 3rd factor accounted for 25.96% of the total variation and is mainly associated with location of fructification, ripe fruit colour, fruit shape and tree crown shape, while fruit shape and tree crown shape showed highest positive correlation. The communality values ranged from 0.49 to 0.13.

According to Table 4, FA identified 5 factors to be retained by the positive eigen value criterion, explained 75.17% of the total genotypes variation and in 5 factor model each character contributed a high percentage variation. FA performed most of the variability of analyzed genotypes are explained by first 3 factors and which together explained 62.05% of the variance among genotypes. First factor with eigen value of 10.44 accounted for 39.65% of

Table 3
Factor loading, Eigen values, cumulative variance, percentage of total (standardized) population of variance explained by five factor model and communalities of the 11 morphological qualitative traits of 100 bullock's heart genotypes from factor analysis

Sr. No.	Morphological qualitative characters	Factor I		Factor II		Factor III		Factor IV		Factor V		Communalities
		UFL	RFL	UFL	RFL	UFL	RFL	UFL	RFL	UFL	RFL	
1.	Tree Crown shape	0.048	0.034	0.171	–0.044	0.242	0.064	0.221	0.395	–0.165	–0.050	0.17
2.	Tree growth habit	–0.409	–0.461	0.118	–0.086	–0.009	0.015	0.084	0.011	0.175	0.098	0.23
3.	Leaf blade shape	–0.193	–0.167	0.325	–0.189	0.096	0.089	–0.105	0.054	0.030	–0.026	0.19
4.	Petal outer colour	0.053	0.034	–0.295	0.376	0.208	–0.008	0.123	0.099	0.031	–0.038	0.16
5.	Location of fructification	0.022	0.022	0.098	–0.116	–0.353	–0.070	0.154	–0.111	0.169	0.407	0.20
6.	Fruit shape	0.191	0.049	0.173	0.019	0.324	0.455	–0.118	0.055	0.199	–0.116	0.23
7.	Fruit symmetry	0.595	0.483	0.350	–0.195	0.019	0.414	0.056	0.114	0.107	0.189	0.49
8.	Uniformity in fruit size	0.663	0.620	–0.117	0.120	–0.010	0.161	0.032	0.011	–0.043	0.048	0.46
9.	Fruit exocarp type	0.092	0.056	–0.492	0.482	0.091	0.002	–0.059	–0.200	0.170	–0.052	0.29
10.	Ripe fruit colour	0.230	0.256	–0.013	–0.163	–0.326	–0.064	–0.114	–0.235	–0.033	0.085	0.18
11.	Pulp texture	–0.021	–0.067	–0.052	0.098	–0.023	–0.045	0.349	0.196	0.058	0.234	0.13
Eigen values		1.10		0.66		0.46		0.26		0.17		–
Total population variance explained (%)		62.70		37.35		25.96		14.91		9.93		–
Cumulative percentage		62.70		100.05		126.01		140.92		150.85		–

Note: UFL– Unrotated Factor Loading; RFL– Rotated Factor Loading and 5 factors will be retained by the positive Eigen value criterion.

the variation and is primarily related to pulp weight, fruit volume, wt. of ripe fruit, fruit wt. at harvest, fruit diameter, pulp%, fruit length, fruit girth and yield, while pulp weight, fruit volume, wt. of ripe fruit, fruit wt. at harvest, fruit pulp%, fruit diameter, fruit length, and fruit girth showed highest positive correlation. Second factor that accounted for 12.90% of the total variance and is mainly loaded by wt. of seeds, no. of seeds/fruit, seed%, seeds:pulp, tree height and leaf length, while wt. of seeds, no. of seeds/fruit, seed%, and seeds:pulp revealed highest positive correlation. Third factor that accounted for 9.50% of the total variation and is mainly associated with rind weight, followed by rind%, receptacle% and fruit pulp%, while fruit rind weight and fruit rind% possessed highest positive correlation. The communality ranged from 0.988 to 0.147.

The data in Table 5 revealed that FA identified 5factors retained by positive eigen value criterion, which explained 97.98% of the total genotypes variation and in 5 factor model each character contributed a high percentage variation. FA performed most of the variability of the analyzed genotypes has been explained by the first 3 factors. First 2 factors extracted which together explained 82.39% of the variance among genotypes. The 1st factor with eigen value of 7.95 accounted for 74.98% of the variation and is primarily related to reducing sugars, total sugars, ascorbic acid and TSS:TA ratio, non-reducing sugars and colour, while reducing sugars, total sugars, ascorbic acid, TSS:TA, non-reducing sugars and colour showed the highest positive correlation with the first factor. The 2nd factor that accounted for 7.41% of the total variance and is mainly loaded by crude fibre followed by non-reducing sugars, titratable acidity and TSS:TA ratio, while crude fibre, non-reducing sugars and titratable acidity revealed the highest positive correlation. The 3rd factor that accounted for 6.69% of the total variation and is mainly associated with carbohydrate followed by texture and non-reducing

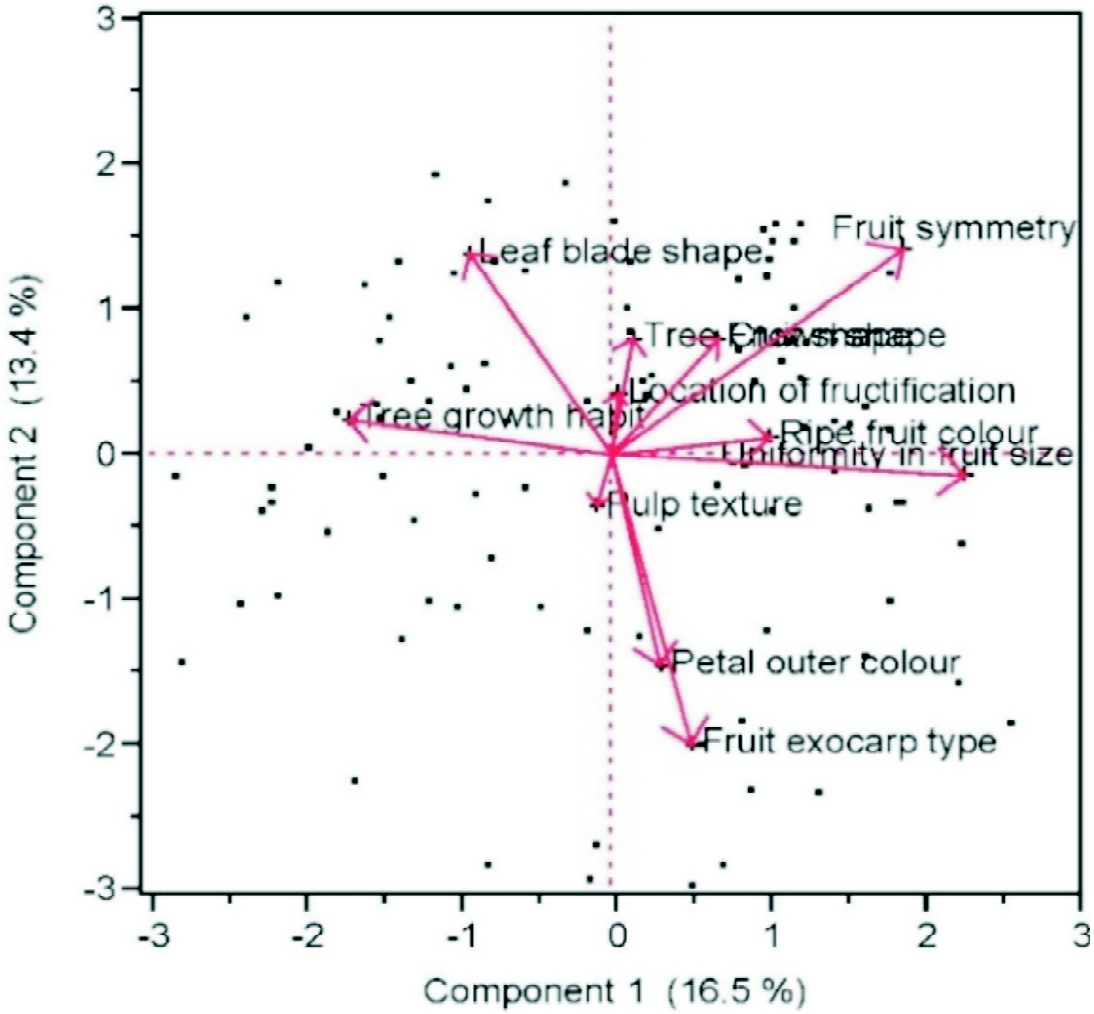

Figure 2: PCA Biplot of PC1 and PC2 factor loadings for genotypes-by-traits and correlation analysis among various morphological qualitative traits

sugars, while carbohydrate and texture possessed highest positive correlation. The communality values ranged from 0.994 to 0.176. These results are more or less in accordance with the observations reported by Manigandan and Vijayakumar, (2014) [9] in *A. muricata*.

Cluster Analysis

According to morphological qualitative data, the germplasm of *A. reticulata* was grouped into eleven distinct clusters on the basis of Ward's minimum distance cluster with each cluster containing accessions that are morphologically similar (Figure 4). Distinct characters were indicated in Table 6. This indicates that the present collection probably contain duplicates. Molecular characterization of these individuals along with morphological characterization will provide the basis for utilization of fruits and conservation of individuals.

Clusters Genotypes and Distinct Characters

I Cluster-I is consisted of fourteen genotypes, SW-1, SW-19, CN-5, SW-8, KL-6, SW-7, DP-5, SW-9, SW-18, KL-4, KN-2, SW-11, DP-12 and DP-13 from Ratnagiri and Sindhudurg districts which had highest mean values for most of the studied traits such as tree growth habit (-1.04), followed by uniformity in fruit size (-0.99) and fruit symmetry (-0.88) and almost lowest for fruit shape (0.18).

II Cluster II comprising of twenty one genotypes, SW-3, SW-12, SW-15, VL-1, VL-18, DP-4, KD-1, VB-4, SW-13, KL-9, VL-16, VL-7, KL-7, DP-10, DP-3, VL-11, VB-2, DP-2, DP-17, VL-19 and VB-1 from Sawantwadi, Vengurla, Vaibhavwadi and Kudal tahsils of Sindhudurg districts and Dapoli and Khed tahsils of Ratnagiri district which had the extreme mean values for location of fructification (0.81).

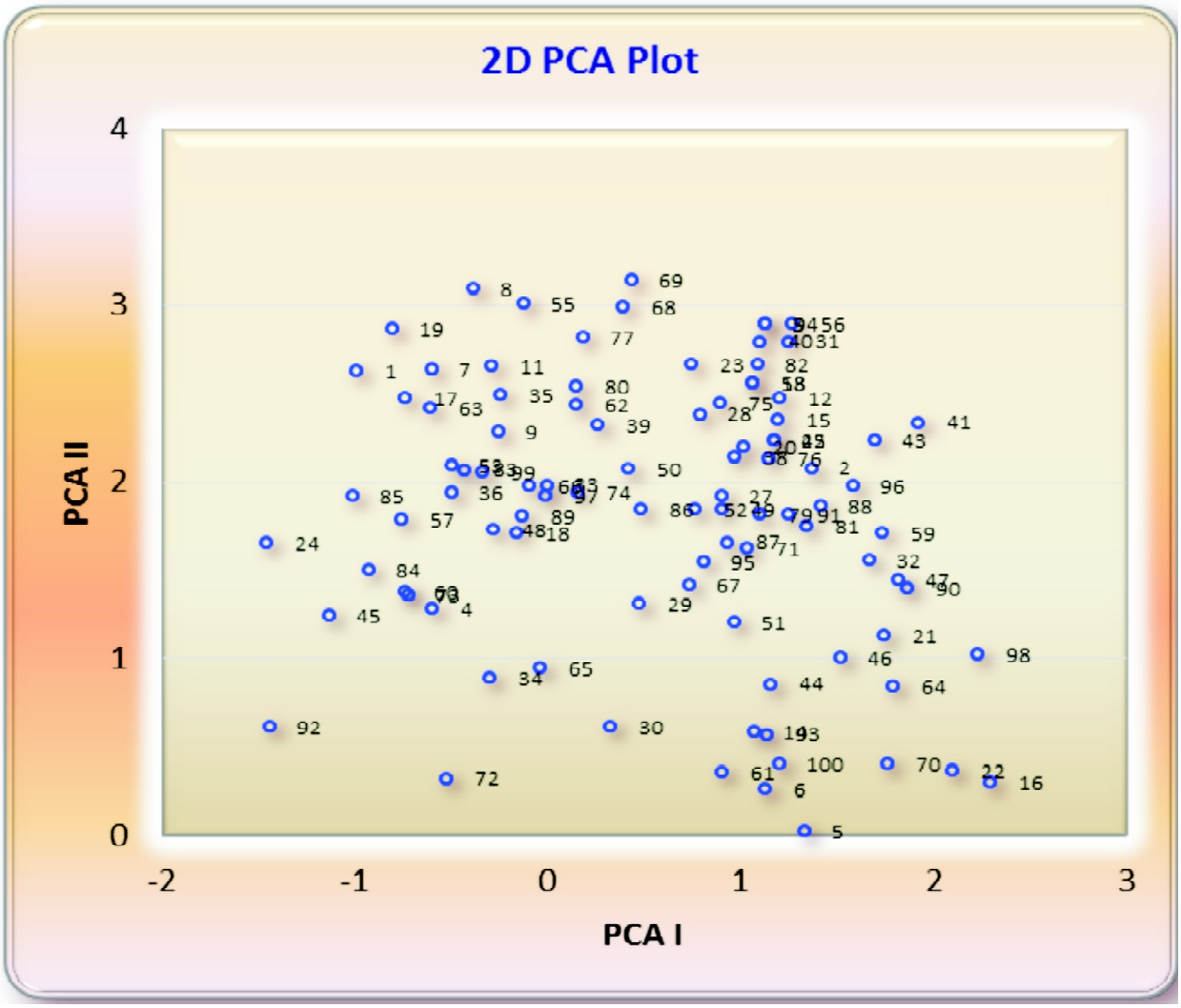

Figure 3: Scattered diagram: 2D ordination showing the relative position of genotypes based on PCA scores (PC 1 and PC 2) of morphological qualitative traits

III Cluster III comprising of four genotypes, VL-5, VL-15, VL-20 and DP-11 from Ratnagiri and Sindhudurg districts which had the extreme mean values for tree crown shape (1.35) and fruit shape (1.33).

IV Cluster IV comprising of eight genotypes, SW-23, VL-4, KN-1, VL-25, CN-2, VL-14, KL-10 and GH-1 from Ratnagiri and Sindhudurg districs which had highest mean values for leaf blade shape (1.73) and location of fructification (1.45) other than tree crown shape (1.35) and fruit shape (1.33).

V Cluster V comprising of five genotypes, SW-2, SW-20, DP-8, KL-3 and DV-4 from Ratnagiri and Sindhudurg districts which had the extreme mean values for fruit shape (2.48) other than tree crown shape (2.50).

VI Cluster VI comprising of seven genotypes, SW-17, VL-21, KL-8, VL-24, DP-14, VB-5 and KD-2 from Ratnagiri and Sindhudurg districts which had the extreme mean values for location of fructification (2.09) other than tree crown shape (3.07), leaf blade shape (3.17) and fruit shape (3.05).

VII Cluster VII comprising of seven genotypes, SW-4, VL-12, SW-24, VL-9, CN-7, DV-3 and VL-10 from Ratnagiri and Sindhudurg districts which had the extreme mean values for ripe fruit colour (2.32) other than leaf blade shape (3.89), tree crown shape (3.64) and fruit shape (3.62) and which were also greater than mean value of all eleven clusters.

VIII Cluster VIII comprising of fourteen genotypes, SW-5, SW-22, VL-2, VL-13, SW-14, VL-6, KL-5, DP-6, SW-21, VL-8, CN-3, DV-1, VB-3 and KL-2 from Ratnagiri and Sindhudurg districts which had possessed first position in case of leaf blade shape (4.61) followed by tree crown shape (4.22) and fruit shape (4.20).

IX Cluster IX comprising of three genotypes, SW-10, MN-2 and VL-22, had almost lowest for fruit symmetry and uniformity in fruit size, no remarkable feature was noticed in this cluster for these two traits, while highest mean values for leaf blade shape (5.33), tree crown shape (4.79) and fruit shape (4.77).

Table 4
Factor loading, Eigen values, cumulative variance and percentage of total (standardized) population of variance explained by five factor model and communalities of 36 morphological quantitative traits of 100 elite bullock's heart genotypes from factor analysis

	Morphological qualitative characters	*Factor I*		*Factor II*		*Factor III*		*Factor IV*		*Factor V*		
Sr. No.		*UFL*	*RFL*	*UFL*	*RFL*	*UFL*	*RFL*	*UFL*	*RFL*	*UFL*	*RFL*	*Communalities*
1.	Canopy spread (m)	0.350	0.447	0.326	0.052	–0.123	0.156	–0.102	–0.084	–0.149	–0.153	0.356
2.	Tree height (m)	0.355	0.474	0.417	0.058	–0.079	0.211	–0.134	–0.112	–0.038	–0.184	0.512
3.	Trunk ramification	–0.047	–0.019	–0.055	–0.042	–0.103	–0.120	–0.072	0.080	–0.276	0.031	0.279
4.	Leaf length (cm)	0.200	0.066	–0.407	0.087	–0.087	–0.178	0.033	0.088	0.757	0.943	0.974
5.	Leaf width (cm)	0.093	–0.022	–0.233	0.081	0.307	–0.098	–0.779	0.934	0.215	0.219	0.971
6.	Leaf length: width ratio (cm)	0.097	0.084	–0.125	0.007	–0.348	–0.049	0.738	–0.777	0.448	0.601	0.984
7.	Leaf Area (cm^2)	0.290	0.207	–0.059	0.165	0.171	–0.046	–0.298	0.199	0.169	–0.015	0.410
8.	Flower length (cm)	–0.036	–0.044	–0.035	–0.016	–0.079	–0.009	0.227	–0.112	–0.022	–0.113	0.309
9.	Flower diameter (cm)	–0.022	–0.066	–0.113	–0.017	0.019	–0.005	0.021	–0.084	0.269	0.057	0.330
10.	Peduncle length [cm]	–0.085	–0.088	–0.171	–0.039	–0.020	–0.199	0.095	–0.148	–0.031	–0.102	0.308
11.	Pedicel length (cm)	–0.036	–0.031	–0.107	–0.057	–0.150	–0.089	0.209	–0.253	–0.087	–0.004	0.165
12.	Petal length (cm)	–0.196	–0.167	0.113	–0.045	0.156	0.069	–0.128	–0.047	–0.160	–0.184	0.341
13.	Petal width (cm)	0.127	0.134	–0.025	0.003	–0.078	–0.046	–0.095	–0.008	0.022	–0.023	0.147
14.	Fruit wt. at harvest	0.932	0.550	–0.054	0.807	0.296	–0.014	0.127	0.041	–0.028	0.042	0.983
15.	Yield (Fruit/tree)	0.501	0.579	0.201	0.087	–0.197	0.022	–0.188	–0.012	–0.026	–0.007	0.467
16.	Fruit length (cm)	0.817	0.821	0.100	0.264	–0.278	–0.094	–0.030	–0.054	0.008	0.078	0.766
17.	Fruit diameter (cm)	0.877	0.886	0.087	0.249	–0.274	–0.095	–0.139	0.040	0.055	0.058	0.886
18.	Fruit girth (cm)	0.814	0.825	0.084	0.224	–0.232	–0.078	–0.195	0.083	0.090	0.073	0.783
19.	Days from harvest to ripening	–0.101	0.037	0.291	–0.119	–0.154	0.176	0.171	–0.075	–0.317	–0.093	0.420
20.	Weight of ripe fruit (gm.)	0.933	0.554	–0.053	0.805	0.293	–0.016	0.124	0.041	–0.032	0.040	0.983
21.	Fruit volume (ml)	0.937	0.559	–0.043	0.806	0.295	–0.009	0.121	0.041	–0.041	0.033	0.988
22.	Specific gravity	–0.751	–0.427	–0.112	–0.729	–0.373	–0.129	–0.082	–0.044	0.079	0.003	0.753
23.	Fruit rind weight (g)	0.462	–0.159	–0.344	0.960	0.749	–0.090	0.238	0.016	–0.105	0.006	0.980
24.	Fruit rind (%)	–0.729	–0.959	–0.376	0.044	0.490	–0.116	0.110	–0.029	–0.082	–0.039	0.976
25.	Fruit rind thickness (mm)	–0.025	0.013	0.101	–0.014	–0.040	0.093	0.179	–0.074	0.198	0.224	0.238
26.	Fruit receptacle length (cm)	0.580	0.565	0.231	0.244	–0.119	0.120	0.054	–0.076	–0.045	–0.021	0.442
27.	Fruit receptacle weight (g)	0.423	0.302	–0.074	0.211	–0.118	0.008	0.106	0.031	–0.307	0.058	0.946
28.	Fruit receptacle (%)	–0.735	–0.380	–0.051	–0.781	–0.459	–0.055	–0.077	–0.035	–0.130	–0.015	0.966
29.	Pulp weight (g)	0.977	0.797	0.035	0.546	–0.034	–0.056	0.031	0.044	0.000	0.054	0.976
30.	Fruit pulp (%)	0.859	0.953	0.130	0.144	–0.429	–0.114	–0.083	0.026	0.025	0.059	0.981
31.	No. of seeds per fruit	0.050	0.069	0.778	0.151	0.333	0.860	0.175	–0.022	0.075	–0.043	0.796
32.	Weight of seeds (g)	0.063	0.131	0.880	0.089	0.336	0.962	0.068	0.024	0.192	–0.063	0.964
33.	Seeds:pulp	–0.758	–0.510	0.562	–0.473	0.160	0.666	–0.008	–0.006	0.147	–0.104	0.954
34.	Seed (%)	–0.605	–0.267	0.746	–0.522	0.038	0.784	–0.045	0.010	0.193	–0.081	0.979
35.	Seed length (cm)	–0.002	0.033	0.048	–0.071	0.102	0.102	–0.248	0.201	0.369	0.174	0.277
36.	Seed width (mm)	0.069	0.062	0.186	0.062	0.050	0.233	0.227	–0.066	0.080	0.017	0.271
Eigen values		10.44		3.40		2.50		1.86		1.59		–
Total population variance explained (%)		39.65		12.90		9.50		7.07		6.05		–
Cumulative percentage		39.65		52.55		62.05		69.12		75.17		–

Note: UFL–Unrotated Factor Loading; RFL–Rotated Factor Loading and 5 factors will be retained by the positive Eigen value criterion.

Table 5
Factor loading, Eigen values, cumulative variance and percentage of total (standardized) population of variance explained by five factor model and communalities of the 18 bio–chemical traits of 100 elite bullock's heart genotypes from factor analysis

Bio-chemical characters		*Factor I*		*Factor II*		*Factor III*		*Factor IV*		*Factor V*		
Sr. No.		*UFL*	*RFL*	*UFL*	*RFL*	*UFL*	*RFL*	*UFL*	*RFL*	*UFL*	*RFL*	*Communalities*
1.	Moisture (%)	0.101	0.034	0.220	–0.023	0.010	0.400	0.041	–0.050	–0.258	0.079	0.176
2.	Total soluble solids (oB)	0.763	0.781	–0.065	–0.067	–0.011	–0.006	0.170	–0.063	0.209	–0.020	0.693
3.	Titratable acidity (%)	–0.815	–0.703	0.357	0.608	–0.248	–0.092	0.171	–0.112	0.147	0.125	0.940
4.	pH	0.234	0.168	0.036	–0.024	0.252	0.034	0.223	–0.147	–0.147	–0.030	0.289
5.	TSS:TA	0.882	0.780	–0.320	–0.539	0.219	0.065	–0.116	0.105	–0.067	–0.081	0.956
6.	Reducing Sugars (%)	0.957	0.960	0.088	–0.068	–0.060	0.102	0.073	–0.029	0.081	0.105	0.976
7.	Non–reducing Sugars (%)	0.827	0.818	0.360	0.229	–0.301	0.460	0.001	0.184	–0.145	–0.013	0.984
8.	Total sugars (%)	0.955	0.954	0.182	0.027	–0.143	0.225	0.052	0.041	0.010	0.070	0.994
9.	Ascorbic acid (mg $100g^{-1}$)	0.886	0.854	–0.066	–0.169	–0.099	0.019	0.099	–0.007	–0.015	0.095	0.857
10.	CHO (%)	–0.038	–0.061	0.114	–0.035	0.373	–0.082	–0.097	–0.034	0.093	0.126	0.235
11.	Protein (%)	–0.056	–0.043	0.190	0.061	0.257	0.048	0.327	–0.428	0.033	0.128	0.235
12.	Crude fibre (%)	0.102	0.060	0.373	0.031	0.166	0.104	–0.169	0.029	0.088	0.479	0.260
13.	Fat (%)	0.082	0.045	0.143	0.026	–0.084	–0.016	–0.520	0.499	0.047	0.232	0.324
14.	Shelf life (days)	0.796	0.829	–0.084	–0.024	–0.130	–0.095	–0.032	0.155	0.240	–0.026	0.735
15.	PLW (%)	–0.581	–0.504	0.127	0.181	0.159	–0.082	0.018	–0.154	0.258	0.022	0.496
16.	Colour	0.819	0.802	–0.068	–0.218	0.012	–0.015	0.044	–0.023	0.186	0.175	0.759
17.	Flavour	0.763	0.647	0.136	–0.175	0.129	0.185	–0.033	0.094	–0.100	0.270	0.710
18.	Texture	0.566	0.474	0.269	–0.169	0.337	0.302	–0.092	–0.005	0.004	0.277	0.545
Eigen values		7.95		0.79		0.71		0.57		0.37		–
Total population variance explained (%)		74.98		7.41		6.69		5.37		3.53		–
Cumulative percentage		74.98		82.39		89.08		94.45		97.98		–

Note: UFL–Unrotated Factor Loading; RFL–Rotated Factor Loading and 5 factors will be retained by the positive Eigen value criterion.

X Cluster X comprising of ten genotypes, VL-17, DP-18, DP-16, CN-4, CN-6, DP-9, VL-23, DP-15, SW-6 and SW-16 from Ratnagiri and Sindhudurg districts which had the extreme mean values for leaf blade shape (6.05), tree crown shape (5.36), fruit shape (5.35), tree growth habit (3.78) and pulp texture (3.77).

XI Cluster XI comprising of seven genotypes, MN-1, DP-1, VL-3, DP-7, CN-1, KL-1 and DV-2 from Ratnagiri and Sindhudurg districts which had the extreme mean values for leaf blade shape (6.76) followed by tree crown shape (5.94) and fruit shape (5.92) and also the remarkable feature was noticed in this cluster for location of fructification, fruit symmetry and uniformity in fruit size.

CONCLUSIONS

Results of the study revealed that five principle components from 11 morphological qualitative, 36 morphological quantitative and 18 bio-chemical characters explained 150.85%, 75.17% and 97.98% of total variability of *A. reticulata* germplasm respectively. Cluster analysis identified eleven clusters with unique characters. Most prominent character is pulp weight contributing most towards variation and this confirmed the pattern of clustering in the morphological quantitative dendrogram. Other characteristics obtained in PCA that determined clustering in the dendrograms were uniformity in fruit size, fruit symmetry, total sugars, Brix/TA ratio, ascorbic acid and shelf life should be given top priority as selection. Variation among genotypes in fruit shape contributed significant positive correlation with fruit symmetry, fruit

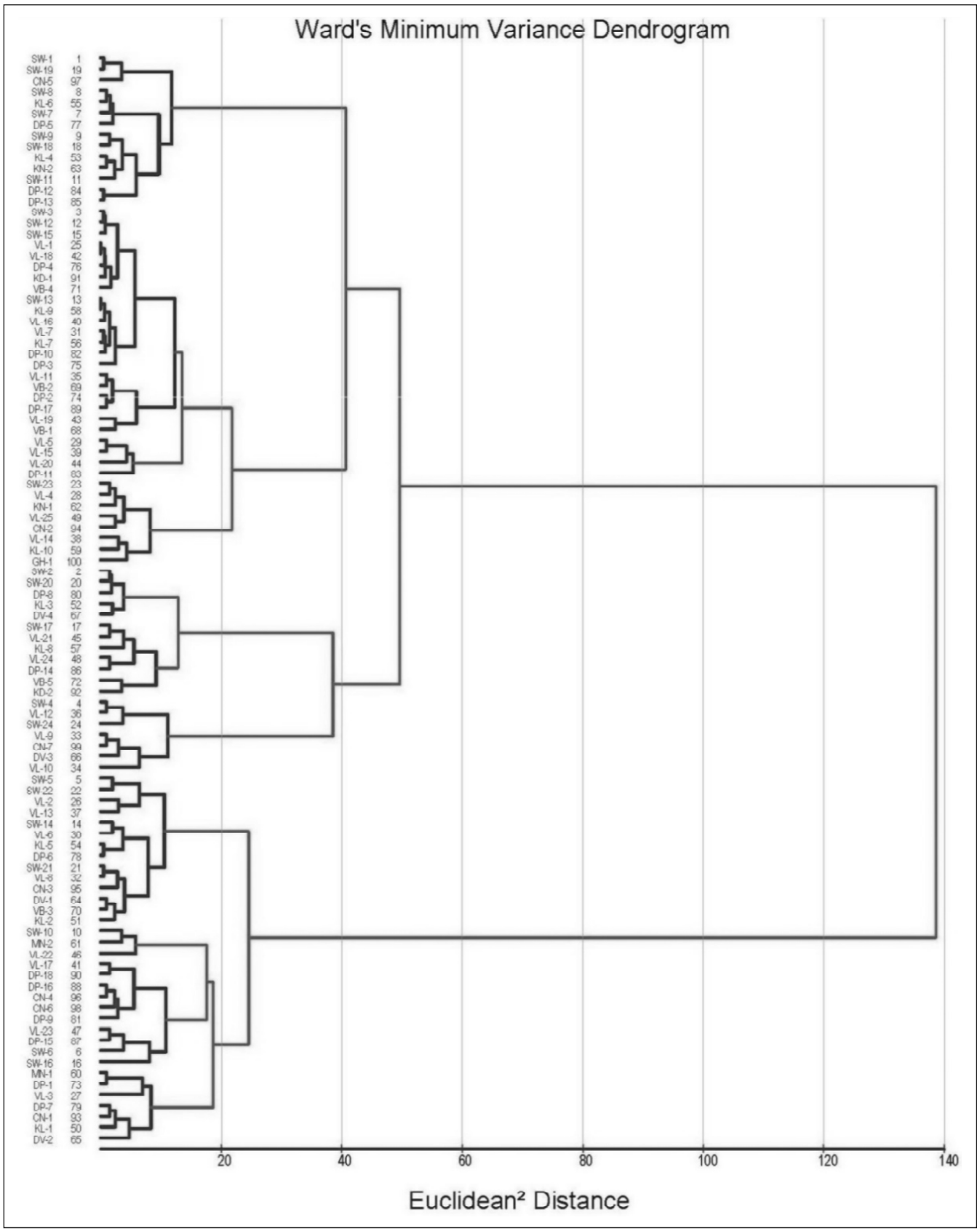

Figure 4: Consensus tree diagram (Dendrogram) representing relationships of 100 elite bullock's heart genotypes produced by Ward's minimum distance cluster analysis based on 11 morphological qualitative traits [Scale: Euclidean² distance]

Table 6
Cluster composition of all genotypes regarding morphological qualitative traits

Clusters	*Genotypes and distinct characters*
I	Cluster-I is consisted of fourteen genotypes, SW-1, SW-19, CN-5, SW-8, KL-6, SW-7, DP-5, SW-9, SW-18, KL-4, KN-2, SW-11, DP-12 and DP-13 from Ratnagiri and Sindhudurg districts which had highest mean values for most of the studied traits such as tree growth habit (-1.04), followed by uniformity in fruit size (-0.99) and fruit symmetry (-0.88) and almost lowest for fruit shape (0.18).
II	Cluster II comprising of twenty one genotypes, SW-3, SW-12, SW-15, VL-1, VL-18, DP-4, KD-1, VB-4, SW-13, KL-9, VL-16, VL-7, KL-7, DP-10, DP-3, VL-11, VB-2, DP-2, DP-17, VL-19 and VB-1 from Sawantwadi, Vengurla, Vaibhavwadi and Kudal tahsils of Sindhudurg districts and Dapoli and Khed tahsils of Ratnagiri district which had the extreme mean values for location of fructification (0.81).
III	Cluster III comprising of four genotypes, VL-5, VL-15, VL-20 and DP-11 from Ratnagiri and Sindhudurg districts which had the extreme mean values for tree crown shape (1.35) and fruit shape (1.33).
IV	Cluster IV comprising of eight genotypes, SW-23, VL-4, KN-1, VL-25, CN-2, VL-14, KL-10 and GH-1 from Ratnagiri and Sindhudurg districs which had highest mean values for leaf blade shape (1.73) and location of fructification (1.45) other than tree crown shape (1.35) and fruit shape (1.33).
V	Cluster V comprising of five genotypes, SW-2, SW-20, DP-8, KL-3 and DV-4 from Ratnagiri and Sindhudurg districts which had the extreme mean values for fruit shape (2.48) other than tree crown shape (2.50).
VI	Cluster VI comprising of seven genotypes, SW-17, VL-21, KL-8, VL-24, DP-14, VB-5 and KD-2 from Ratnagiri and Sindhudurg districts which had the extreme mean values for location of fructification (2.09) other than tree crown shape (3.07), leaf blade shape (3.17) and fruit shape (3.05).
VII	Cluster VII comprising of seven genotypes, SW-4, VL-12, SW-24, VL-9, CN-7, DV-3 and VL-10 from Ratnagiri and Sindhudurg districts which had the extreme mean values for ripe fruit colour (2.32) other than leaf blade shape (3.89), tree crown shape (3.64) and fruit shape (3.62) and which were also greater than mean value of all eleven clusters.
VIII	Cluster VIII comprising of fourteen genotypes, SW-5, SW-22, VL-2, VL-13, SW-14, VL-6, KL-5, DP-6, SW-21, VL-8, CN-3, DV-1, VB-3 and KL-2 from Ratnagiri and Sindhudurg districts which had possessed first position in case of leaf blade shape (4.61) followed by tree crown shape (4.22) and fruit shape (4.20).
IX	Cluster IX comprising of three genotypes, SW-10, MN-2 and VL-22, had almost lowest for fruit symmetry and uniformity in fruit size, no remarkable feature was noticed in this cluster for these two traits, while highest mean values for leaf blade shape (5.33), tree crown shape (4.79) and fruit shape (4.77).
X	Cluster X comprising of ten genotypes, VL-17, DP-18, DP-16, CN-4, CN-6, DP-9, VL-23, DP-15, SW-6 and SW-16 from Ratnagiri and Sindhudurg districts which had the extreme mean values for leaf blade shape (6.05), tree crown shape (5.36), fruit shape (5.35), tree growth habit (3.78) and pulp texture (3.77).
XI	Cluster XI comprising of seven genotypes, MN-1, DP-1, VL-3, DP-7, CN-1, KL-1 and DV-2 from Ratnagiri and Sindhudurg districts which had the extreme mean values for leaf blade shape (6.76) followed by tree crown shape (5.94) and fruit shape (5.92) and also the remarkable feature was noticed in this cluster for location of fructification, fruit symmetry and uniformity in fruit size.

symmetry with uniformity in fruit size and fruit colour, uniformity in fruit size with fruit exocarp type and exocarp colour, while yield had significant positive correlation with fruit length, diameter, girth, weight, pulp weight, pulp% and no. of seed. These factors are important in utilization of the fruit. Therefore, clusters which have higher and lower pulp weight to seed ratio are important to promote for utilization of breeding programmes and conservation of germplasms. Factor analysis captured more of the variation within the genotypes as compared to other.

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